

GenCore version 5.1.4\_p5\_4578  
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## OM protein - protein search, using sw model

Run on: May 19, 2003, 16:43:18 ; Search time 29.0436 Seconds

(without alignments)  
1237.942 Million cell updates/sec

Title: US-09-625-573-2

Perfect score: 1970  
Sequence: 1 MLSTSRSRFIRNTNESGEVY.....GKGSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

FIR\_73-\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

## RESULT 1

I38450

Chemokine (C-C) receptor 2, splice form A - human

N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte

C;Species: Homo sapiens (man)

C;Date: 16-Feb-1996 #sequence\_change 13-Aug-1999

C;Accession: I38450

R;Charo, I.F.; Myers, S.J.; Herman, A.; Connolly, C.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994

A;Title: Molecular cloning and functional expression of two monocyte chemoattractant

A;Reference number: A53477; MUID:94195821; PMID:8146186

A;Accession: I38450

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 &lt;RES&gt;

A;Cross-references: EMBL:U03882; PIDN:AAAI9119.1; PIDN:9472556

A;Gene: CHMRB2

A;Cross-references: GDB:337364; OMIM:601267

A;Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane

F;44-68/Domain: transmembrane #status predicted &lt;TM1&gt;

F;79-99/Domain: transmembrane #status predicted &lt;TM2&gt;

F;115-136/Domain: transmembrane #status predicted &lt;TM3&gt;

F;154-178/Domain: transmembrane #status predicted &lt;TM4&gt;

F;208-226/Domain: transmembrane #status predicted &lt;TM5&gt;

F;244-265/Domain: transmembrane #status predicted &lt;TM6&gt;

F;292-309/Domain: transmembrane #status predicted &lt;TM7&gt;

F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;32-277,113-190/disulfide bonds: #status predicted

Query Match

100.0%; Score 1970; DB 2;

Best Local Similarity 100.0%; Pred. No.

Matches 374; Conservative 0; Indels 0; Gaps 0;

Qy 1 MLSTSRFSRINTNESGEVTTFFDYYGAPCKFDVKQIGAQALPLPLSVEFGFGVN 60

Db 1 MLSTSRSRFSRINTNESGEVTTFFDYYGAPCKFDVKQIGAQALPLPLSVEFGFGVN 60

Qy 61 MLVVLILINCKKLCKLTDIYLLNLAISDLFLFLTLPWLSAANENVFGNAMCKLEFTGLY 120

Db 61 MLVVLILINCKKLCKLTDIYLLNLAISDLFLFLTLPWLSAANENVFGNAMCKLEFTGLY 120

Qy 121 HIGYEGGIFEFFLTLIDRYLAIHVAYEALKARTVTGFGVTSVTVLIVAVFASVPGITFK 180

Db 121 HIGYEGGIFEFFLTLIDRYLAIHVAYEALKARTVTGFGVTSVTVLIVAVFASVPGITFK 180

Qy 181 CQKEDSYVVCGVDFPGRWNHHTIMRNFLGVLIMVCGSIKLTLLCRNEKKRR 240

Db 181 CQKEDSVVYVGPFPGRWNNHHTIMRNFLGVLIMVCGSIKLTLLCRNEKKRR 240

|  |    |       |      |     |   |                    |
|--|----|-------|------|-----|---|--------------------|
|  | 30 | 519   | 26.3 | 333 | 2 | I65989             |
|  | 31 | 484   | 24.6 | 359 | 2 | JN0621             |
|  | 32 | 480   | 24.4 | 359 | 2 | A42656             |
|  | 33 | 479.5 | 24.3 | 374 | 2 | S42628             |
|  | 34 | 475   | 24.1 | 359 | 2 | I51372             |
|  | 35 | 473   | 24.0 | 359 | 2 | JC2134             |
|  | 36 | 472   | 24.0 | 359 | 2 | JH0621             |
|  | 37 | 471   | 23.9 | 359 | 2 | angiotensin II rec |
|  | 38 | 471   | 23.9 | 359 | 2 | angiotensin II rec |
|  | 39 | 469   | 23.8 | 359 | 2 | JC1104             |
|  | 40 | 468   | 23.8 | 359 | 2 | S44425             |
|  | 41 | 465   | 23.6 | 359 | 2 | JC1194             |
|  | 42 | 465   | 23.6 | 374 | 2 | S32785             |
|  | 43 | 464   | 23.6 | 359 | 2 | MDCR15 protein - h |
|  | 44 | 461.5 | 23.4 | 372 | 2 | S26667             |
|  | 45 | 460.5 | 23.4 | 327 | 2 | S56162             |

## ALIGNMENTS

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description                                       |
|------------|--------|-------------|--------|----|---|
| 1          | 1970   | 100.0       | 374    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 2          | 1651.5 | 83.8        | 360    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 3          | 1224   | 62.1        | 352    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 4          | 967.5  | 49.1        | 355    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 5          | 960    | 48.7        | 359    | 2  | MIP-1 alpha receptor                              |
| 6          | 902.5  | 45.8        | 355    | 2  | macrophage inflammatory protein-1 receptor        |
| 7          | 890.5  | 45.2        | 355    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 8          | 833    | 42.3        | 360    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 9          | 831.5  | 42.2        | 360    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 10         | 794.5  | 40.3        | 383    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 11         | 731    | 37.1        | 356    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 12         | 723    | 36.7        | 355    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 13         | 704.5  | 35.8        | 354    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 14         | 698    | 35.4        | 355    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 15         | 644.5  | 32.7        | 344    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 16         | 584    | 29.6        | 378    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 17         | 575.5  | 29.2        | 378    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 18         | 570    | 28.9        | 378    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 19         | 554.5  | 28.1        | 369    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 20         | 541.5  | 27.5        | 360    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 21         | 537    | 27.3        | 359    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 22         | 531    | 27.0        | 352    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 23         | 529.5  | 26.9        | 353    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 24         | 529.5  | 26.9        | 355    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 25         | 528    | 26.8        | 352    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 26         | 526    | 26.7        | 358    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 27         | 526    | 26.7        | 367    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 28         | 524.5  | 26.6        | 350    | 2  | chemokine (C-C) receptor 2, splice form A - human |
| 29         | 523    | 26.5        | 356    | 2  | chemokine (C-C) receptor 2, splice form A - human |

|    |     |  |     |    |     |   |     |
|----|-----|--|-----|----|-----|---|-----|
| Qy | 241 | AVRVFTIMIVYFLEWTNPVNIVLNTFOEFFGLSNCESTSQLDOATOVDETLGMTHCCII  | 300 | Qy | 241 | AVRVFTIMIVYFLEWTNPVNIVLNTFOEFFGLSNCESTSQLDOATOVDETLGMTHCCII | 300 |
| Db | 241 | AVRVFTIMIVYFLEWTNPVNIVLNTFOEFFGLSNCESTSQLDOATOVDETLGMTHCCII  | 300 | Db | 241 | AVRVFTIMIVYFLEWTNPVNIVLNTFOEFFGLSNCESTSQLDOATOVDETLGMTHCCII | 300 |
| Qy | 301 | NPIIYAFGEKFRSLFHIALGCRAPLKQEVCGGPVVRPKVKVTTQGLLDGRGKGSII   | 360 | Qy | 301 | NPIIYAFGEKFR - -SLF-- -HIALG-ORIAPL                         | 327 |
| Db | 301 | NPIIYAFGEKFRSLFHIALGCRAPLKQEVCGGPVVRPKVKVTTQGLLDGRGKGSII   | 360 | Db | 301 | NPIIYAFGEKFRYSVEFKRHKRKCQCPV                                | 334 |
| Qy | 361 | GRAPEASLQDKEGA   | 374 |    |     |   |     |
| Db | 361 | GRAPEASLQDKEGA   | 374 |    |     |   |     |
|    |     | RESULT 3   |     |    |     |   |     |
|    |     | A43113   |     |    |     |   |     |
|    |     | chemokine (C-C) receptor 5 - human   |     |    |     |   |     |
|    |     | N;Alternate names: C-C CKR-5; CCR5   |     |    |     |   |     |
|    |     | C;Species: Homo sapiens (man)  |     |    |     |   |     |
|    |     | C;Accession: A43113; S71808; A58834; G0253; A58833   |     |    |     |   |     |
|    |     | C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000  |     |    |     |   |     |
|    |     | C;Accession: JC2443; U038463   |     |    |     |   |     |
|    |     | A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor 5                        |     |    |     |   |     |
|    |     | A;Reference number: A43113; MUID:96241590; PMID:8639485  |     |    |     |   |     |
|    |     | A;Accession: A43113  |     |    |     |   |     |
|    |     | A;Molecule type: mRNA  |     |    |     |   |     |
|    |     | A;Residues: 1-360 <YAM>  |     |    |     |   |     |
|    |     | A;Cross-references: DBI:D29984; NID:9531246; PIDN:BA006253; 1; PID:9531247   |     |    |     |   |     |
|    |     | R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.                                 |     |    |     |   |     |
|    |     | Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  |     |    |     |   |     |
|    |     | A;Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1                     |     |    |     |   |     |
|    |     | A;Reference number: A53477; MUID:94195821; PMID:8416186  |     |    |     |   |     |
|    |     | A;Status: preliminary  |     |    |     |   |     |
|    |     | A;Molecule type: mRNA  |     |    |     |   |     |
|    |     | A;Residues: 1-360 <RES>  |     |    |     |   |     |
|    |     | A;Cross-references: EMBL:U03905; PIDN:AAA19120..1; PID:9472558   |     |    |     |   |     |
|    |     | C;Genetics:  |     |    |     |   |     |
|    |     | A;Gene: GDB:CMKBR2   |     |    |     |   |     |
|    |     | A;Cross-references: GDB:337364; OMIM:601267  |     |    |     |   |     |
|    |     | A;Map position: 3p21-p21   |     |    |     |   |     |
|    |     | C;Superfamily: vertebrate rhodopsin  |     |    |     |   |     |
|    |     | C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane                          |     |    |     |   |     |
|    |     | F:43-70/Domain: transmembrane #status predicted <TM1>  |     |    |     |   |     |
|    |     | F:81-100/Domain: transmembrane #status predicted <TM3>   |     |    |     |   |     |
|    |     | F:115-136/Domain: transmembrane #status predicted <TM3>  |     |    |     |   |     |
|    |     | F:154-178/Domain: transmembrane #status predicted <TM4>  |     |    |     |   |     |
|    |     | F:207-226/Domain: transmembrane #status predicted <TM5>  |     |    |     |   |     |
|    |     | F:244-268/Domain: transmembrane #status predicted <TM6>  |     |    |     |   |     |
|    |     | F:287-309/Domain: transmembrane #status predicted <TM7>  |     |    |     |   |     |
|    |     | F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted   |     |    |     |   |     |
|    |     | F:113-190/Disulfide bonds: #status predicted   |     |    |     |   |     |
|    |     | Query Match Score 83.8%; Best Local Similarity 95.5%; Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3; |     |    |     |   |     |
| Qy | 1   | M1STSRSRFINTNESGEVTFDYDGYAPCKFDVKQIGAQOLLPLPLSYLVIFGFVGN   | 60  | Qy | 1   | M1VLLILINCKKLCKLTDYLNLNAISDLFLFLITPLWAHSAAANEVFGNAMCKLFGLY  | 120 |
| Db | 1   | M1STSRSRFINTNESGEVTFDYDGYAPCKFDVKQIGAQOLLPLPLSYLVIFGFVGN   | 60  | Db | 1   | M1VLLILINCKKLCKLTDYLNLNAISDLFLFLITPLWAHSAAANEVFGNAMCKLFGLY  | 120 |
| Qy | 61  | MLVLLILINCKKLCKLTDYLNLNAISDLFLFLITPLWAHSAAANEVFGNAMCKLFGLY   | 120 | Qy | 61  | MLVLLILINCKKLCKLTDYLNLNAISDLFLFLITPLWAHSAAANEVFGNAMCKLFGLY  | 120 |
| Db | 61  | MLVLLILINCKKLCKLTDYLNLNAISDLFLFLITPLWAHSAAANEVFGNAMCKLFGLY   | 120 | Db | 61  | MLVLLILINCKKLCKLTDYLNLNAISDLFLFLITPLWAHSAAANEVFGNAMCKLFGLY  | 120 |
| Qy | 121 | HIGYFGGIFTILLTDRYLAIHVAYFALKARTVTFGVVTWVAVFASVPGLIFTK  | 180 | Qy | 121 | HIGYFGGIFTILLTDRYLAIHVAYFALKARTVTFGVVTWVAVFASVPGLIFTK       | 180 |
| Db | 121 | HIGYFGGIFTILLTDRYLAIHVAYFALKARTVTFGVVTWVAVFASVPGLIFTK  | 180 | Db | 121 | HIGYFGGIFTILLTDRYLAIHVAYFALKARTVTFGVVTWVAVFASVPGLIFTK       | 180 |
| Qy | 181 | QKEKSVYYCCPYFPRGWNNTHTMNLGVLPLIMVICYSGILKTLICRNEKKRRH  | 240 | Qy | 181 | QKEKSVYYCCPYFPRGWNNTHTMNLGVLPLIMVICYSGILKTLICRNEKKRRH       | 240 |
| Db | 181 | QKEKSVYYCCPYFPRGWNNTHTMNLGVLPLIMVICYSGILKTLICRNEKKRRH  | 240 | Db | 181 | QKEKSVYYCCPYFPRGWNNTHTMNLGVLPLIMVICYSGILKTLICRNEKKRRH       | 240 |

A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RA

A; Note: probably acts to control granulocyte proliferation and differentiation  
 C; Superfamily: vertebrate rhodopsin  
 C; Keywords: ADRS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane  
 F; 32-56/Domain: transmembrane #status predicted <TM1>  
 F; 67-87/Domain: transmembrane #status predicted <TM2>  
 F; 103-124/Domain: transmembrane #status predicted <TM3>  
 F; 142-166/Domain: transmembrane #status predicted <TM4>  
 F; 193-218/Domain: transmembrane #status predicted <TM5>  
 F; 236-257/Domain: transmembrane #status predicted <TM6>  
 F; 285-300/Domain: transmembrane #status predicted <TM7>  
 F; 288-309-101-178/Disulfide bonds: #status predicted  
 F; 288/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F; 336-337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
 F; 340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 62.1%; Score 1224; DB 2; Length 352;  
 Best Local Similarity 76.3%; Pred. No. 4.8e-101;  
 Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3; ,  
 Query 24 FDYD--GAPCHKFDVQIGAQQLPPLSVLTFGVGNMVLVLLINRKLCRKLTDIVL 81  
 Db 10 YDINYTYSEPCQKINVQTAARLPLPLSVLTFGVGNMVLVLLINRKLSMTDIVL 69  
 Query 82 LNLAISDLFLFLITPLWLAHSANNEWFGNAMCKLFTGLYHIGYEGGIFFLILLTIDRYLA 141  
 Db 70 LNLAISDLFLFLTTLVPEWHAHAAWQDGNMQLLTGIGFEGSGIFFLILLTIDRYLA 129  
 Query 142 IVHAVFAALKARTVTFGVTTSVITLVAVATASVPGTITTCQKEDSVYVGPFYFP---RG 197  
 Db 130 VVHAVFAALKARTVTFGVTTSVITWAVAVASLPGTITFSQKEGHYTCSSSHFYSQYQF 189  
 Query 198 WNNFHFTIMRNILGVLPLLIMVYCGILKTLLCRNEKKRRAVFTIMIYFLFWT 257  
 Db 190 WKNFQTLLKIVLGLVPLLVWICYSGLIKTLLCRNEKKRRAVRLITTIMIYFLFWA 249  
 Query 258 PYNIVLLNTFOEFFGLNSCESTSOLDAQTVTEFLGMTHCCINPIIYAFGEKERSLF - 316  
 Db 250 PYNIVLLNTFOEFFGLNCCSSSNRLQAMQVTEFLGMTHCCINPIIYAFGEKERNYL 309  
 Query 317 ----HIA 319  
 Db 310 VFFQKHA 317

## RESULT 4

A45177 chemokine (C-C) receptor 1 - human  
 N; Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor  
 C; Species: Homo sapiens (man)  
 C; Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
 C; Accession: A45177; 15561  
 R; Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.  
 Cell 72, 415-425, 1993  
 A; Title: Molecular cloning, functional expression, and signaling characteristics of a C-  
 A; Reference number: A45177; MUID:93161416; PMID:7679328  
 A; Accession: A45177  
 A; Status: nucleic acid sequence not shown  
 A; Molecule type: mRNA  
 A; Residues: 1-355 <NEO>  
 A; Cross-references: GB:L10918; NID:9292416; PID:9292417  
 A; Experimental source: HL60 cells  
 A; Note: sequence extracted from NCBI backbone (NCBIP:124876)  
 R; Gao, J.  
 J. Exp. Med. 177, 1421-1427, 1993  
 A; Title: Structure and functional expression of the human macrophage inflammatory 1 alpha  
 A; Reference number: 155671; MUID:93240122; PMID:7883036  
 A; Accession: I55671  
 A; Status: preliminary; translated from GB/EMBL/DDBJ  
 A; Molecule type: mRNA  
 A; Residues: 1-355 <RBS>  
 A; Cross-references: GB:L10918; NID:9292416; PID:9292417  
 C; Genetics:  
 A; Gene: GDB:CMKBR1; CMKR-1

A; Cross-references: GDB:138446; OMIM:601159  
 A; Map position: 3p21.3p21  
 C; Superfamily: vertebrate rhodopsin  
 C; Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane  
 F; 36-60/Domain: transmembrane #status predicted <TM1>  
 F; 71-91/Domain: transmembrane #status predicted <TM2>  
 F; 108-129/Domain: transmembrane #status predicted <TM3>  
 F; 147-171/Domain: transmembrane #status predicted <TM4>  
 F; 205-223/Domain: transmembrane #status predicted <TM5>  
 F; 240-264/Domain: transmembrane #status predicted <TM6>  
 F; 288-305/Domain: transmembrane #status predicted <TM7>  
 F; 5/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F; 24-273,106-183/Disulfide bonds: #status predicted  
 F; 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
 F; 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 49.1%; Score 967.5; DB 2; Length 355;  
 Best Local Similarity 58.7%; Pred. No. 2.9e-8;  
 Matches 185; Conservative 47; Mismatches 72; Indels 11; Gaps 5;

Query 12 NTNESEEEVTTFFDYGDATPQKVNERAQGAQLPPLSVLTFGVGNMVLVLLINLK 71  
 Db 5 NTTED-YDTTTEFDIGDATPQKVNERAQGAQLPPLSVLTFGVGNMVLVLLVQYK 63  
 Query 72 KLKCCLTDIYLNLASDLFLFLITPLW - HSAANENWFGNAMCKLFTGLYHIGYFCGIFF 130  
 Db 64 RLKNMITSIYLNLASDLFLFLTLPWIDYKLKDDDNVFGDAMCKLISGFYTGLYSEIFF 123  
 Query 72 KLKCCLTDIYLNLASDLFLFLITPLW - HSAANENWFGNAMCKLFTGLYHIGYFCGIFF 130  
 Db 64 RLKNMITSIYLNLASDLFLFLTLPWIDYKLKDDDNVFGDAMCKLISGFYTGLYSEIFF 123  
 Query 131 IILLTIDRYLAIVAHYFALKARTVTFGVYTSTVITWAVFASVPGTITFTCQKEDSYVYC 190  
 Db 124 IILLTIDRYLAIVAHYFALKARTVTFGVYTSTVITWAVFASVPGTITFTCQKEDSYVYC 183  
 Query 191 GPYFP -- RGWNINFHTIMRNILGVLPLLIMVYCGILKTLLCRNEKKRRAVRFV 246  
 Db 184 SLHFPESELREWKLQFQALKLNLFGLVPLVWICYTGTGILKILRSPNEKK - SKAVRLIF 242  
 Query 247 TIMIYFLFWTPYVNLVLLNTFQEFFGLNSCESTSOLDAQTVTEFLGMTHCCINPLIYA 306  
 Db 243 VIMMIFLFWTPYVNLVLLISVFLQDFLETHEQSRRHLDLAVQTVTEVAYTHCCVNPVIYA 302  
 Query 307 FVGEKF---RSLFH 317  
 Db 303 FVGERFRKYLRQLFH 317

## RESULT 5

A45341 I49341  
 MIP-1 alpha receptor like-2 - mouse  
 C; Species: Mus musculus (house mouse)  
 C; Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 02-Jul-1998  
 C; Accession: I49341  
 R; Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995  
 A; Title: Cloning and differential tissue-specific expression of three mouse beta ch-  
 A; Reference number: 149339; MUID:95340546; PMID:7542241  
 A; Accession: I49341  
 A; Status: preliminary; translated from GB/EMBL/DDBJ  
 A; Molecule type: DNA  
 A; Residues: 1-359 <RE>  
 A; Cross-references: EMBL:028406; NID:9881551; PID:9881552  
 C; Superfamily: vertebrate rhodopsin

Query Match 48.7%; Score 960; DB 2; Length 359;  
 Best Local Similarity 50.1%; Pred. No. 1.4e-77;  
 Matches 187; Conservative 59; Mismatches 89; Indels 38; Gaps 7;

Query 10 IRNTNESGEETTFFDYGDAPCHKFDVKQIGAQLPPLSVLTFGVGNMVLVLLIN 69  
 Db 8 IKTVVSEF--TTPYEVEWAPCEKVRIKEGLSWLPPLYSVFTLGQNMVVLILIK 65  
 Query 70 CKRLKCTDIYLNLASDLFLFLITPLDUWAHAA - NEWVFGNAMCKLFTGLYHIGYFCGI 128  
 Db 66 YRKQIMTNIXYLENLASDLFLFLTVFWIHYVLLNEWMGFGHYNMCKMLSGFYALYSEI 125

Qy 129 FFILLTIDRYLAIVHAFLKARTVTGTVTSVITLVAFFASVPGILIFTKQKEDSVY 188 C; Accession: G02436; A57237  
 Db 126 FFILLTIDRYLAIVHAFLKARTVTGTVTSVITLVAFFASVPGILIFTKQKEDSVY 185 R; Ponath, P.D.  
 Submitted to the EMBL Data Library, February 1995  
 A; Reference number: HO1272  
 A; Status: translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 1-355 <PON>  
 A; Cross-references: EMBL:U49727; NID:91477560; PIDN:AAB09726\_1; PID:91477561  
 R; Combadiere, C.; Ahuja, S.K.; Murphy, P.M.  
 J. Biol. Chem. 270, 16491-16494, 1995  
 A; Title: Cloning and functional expression of a human eosinophil CC chemokine receptor  
 A; Reference number: A57237; MUID:95348056; PMID:7622448  
 A; Status: nucleic acid sequence not shown  
 A; Molecule type: mRNA  
 A; Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>  
 A; Cross-references: GB:U288634; NID:91199579; PIDN:AC50469\_1; PID:91199580  
 A; Note: the translated sequence in GenBank entry HSU288694, release 113.0, PMID: AAC504  
 C; Genetics:  
 A; Gene: CMKB3  
 A; Cross-references: GDB:579624; OMIM:601268  
 A; Map Position: 3p21-3p21  
 C; Superfamily: vertebrate rhodopsin  
 C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane  
 F; 36-50/Domain: transmembrane #status predicted <TM1>  
 F; 71-91/Domain: transmembrane #status predicted <TM2>  
 F; 147-171/Domain: transmembrane #status predicted <TM3>  
 F; 205-23/Domain: transmembrane #status predicted <TM4>  
 F; 240-261/Domain: transmembrane #status predicted <TM5>  
 F; 288-305/Domain: transmembrane #status predicted <TM6>  
 F; 24-273, 106-18/Disulfide bonds: #status predicted <TM7>  
 F; 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
 Query Match 45.28; Score 890.5; DB 2; Length 355;  
 Best Local Similarity 54.6%; Pred. No. 2e-71;  
 Matches 167; Conservative 56; Mismatches 72; Indels 11; Gaps 5;

Qy 149339 Macrophage inflammatory protein-1 alpha receptor - mouse  
 C; Species: Mus musculus (house mouse)  
 C; Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
 A; Accession: I49339  
 R; Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995  
 A; Title: Cloning and differential tissue-specific expression of three mouse beta chemoki  
 A; Reference number: I49339; MUID:95340546; PMID:7542241  
 A; Accession: I49339  
 A; Status: preliminary; translated from GB/EMBL/DDJB  
 A; Molecule type: DNA  
 A; Residues: 1-355 <RES>  
 A; Cross-references: EMBL:U28404; NID:9881547; PIDN:AAA89153\_1; PID:9881548  
 C; Superfamily: vertebrate rhodopsin  
 Query Match 45.8%; Score 902.5; DB 2; Length 355;  
 Best Local Similarity 53.1%; Pred. No. 1.7e-22;  
 Matches 170; Conservative 58; Mismatches 75; Indels 17; Gaps 6;

Qy 21 TTEFDYDYGACHKFDVKQIGAQQLPLPVLYFIFGVNMVYLINCKLKCLTDIY 80  
 Db 13 TTEFDYGDSTPCQKTAVRAFGAGLPLPVLYFIFGVNMVYLINCKLKCLTDIY 72  
 Qy 81 LLNLATSDLLFLTLPWHA-S-ANERVFGNAMCKLFTGLYHIGFCGTCFFILLTIDRY 139  
 Db 73 LNLNAFLDLSLFLTLPWHA-S-ANERVFGNAMCKLFTGLYHIGFCGTCFFILLTIDRY 139  
 Qy 73 LNLNAFLDLSLFLTLPWHA-S-ANERVFGNAMCKLFTGLYHIGFCGTCFFILLTIDRY 139  
 Db 140 LATIVHAVFLAKARTVTGTVTSVITLVAFFASVPGILIFTKQKEDSVYCCGPYFP---- 195  
 Qy 133 LATIVHAVFLAKARTVTGTVTSVITLVAFFASVPGILIFTKQKEDSVYCCGPYFP---- 195  
 Db 133 LATIVHAVFLAKARTVTGTVTSVITLVAFFASVPGILIFTKQKEDSVYCCGPYFP---- 195  
 Qy 196 RGWNNFHTIMRNLLGVLPLPVLYFIFGVNMVYLINCKLKCLTDIY 192  
 Db 193 RGWNNFHTIMRNLLGVLPLPVLYFIFGVNMVYLINCKLKCLTDIY 192  
 Qy 193 KQWKREQALKLNLLGVLPLVMICAGIRILLR-RPSKKVAVRLIPFAITLFL 251  
 Db 193 KQWKREQALKLNLLGVLPLVMICAGIRILLR-RPSKKVAVRLIPFAITLFL 251  
 Qy 256 WTPYNVILNTEQQEFGSLNESTSOLDQATQVTEITLGMTHCCINPIIYAVGEKF-- 312  
 Db 252 WTPYNVILNTEQQEFGSLNESTSOLDQATQVTEITLGMTHCCINPIIYAVGEKF-- 312  
 Qy 313 -RSLF-HIALGCRAPLQK 329  
 Db 312 LRHFFH 317  
 RESULT 8  
 JC4587  
 chemokine (C-C) receptor 4 - mouse  
 C; Species: Mus musculus (house mouse)  
 C; Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000  
 C; Accession: JC4587  
 R; Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996  
 A; Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines

RESULT 7  
 G02436  
 Chemokine (C-C) receptor 3 - human  
 N; Alternate names: C-C CKR-3  
 C; Species: Homo sapiens (man)  
 C; Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 04-Mar-2000



QY 296 THCCINPIIYAFYGEKFR ---SLFHIALG---CRIAPLQKPVCGPGVYRGKPNVKVTIQ 348  
 Db 331 THCCINPIIYAFYGEKFRHLHYFFHTYYATIYLCKYIP----- 368

QY 349 GLLDGRGKGR 358  
 Db 369 -FLSGDGEKG 377

**RESULT 11**  
 I49340 M1P-1 alpha receptor like-1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
 C:Accession: 149340  
 R:Gao, J.L.; Murphy, P.M.  
 J: Biol. Chem. 270, 17494-17501, 1995  
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine  
 A:Reference number: 149339; MUID:95340546; PMID:7542241  
 A:Accession: I49340  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-355 <BOND>  
 A:Cross-references: EMBL:U5983; NID:91245056; PID:91468979  
 C:Comment: This protein belongs to the family of beta chemokine receptors.  
 C:Genetics:  
 A:Gene: GDB CMKBR8; CMKBR2; TER1; CKR-L1  
 A:Cross-references: GDB:6053733; OMIM:601834  
 A:Map position: 3p21-3p21  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; transmembrane protein  
 F:36-63/Domain: transmembrane #status predicted <TM1>  
 F:73-94/Domain: transmembrane #status predicted <TM2>  
 F:108-129/Domain: transmembrane #status predicted <TM3>  
 F:147-171/Domain: transmembrane #status predicted <TM4>  
 F:200-222/Domain: transmembrane #status predicted <TM5>  
 F:239-260/Domain: transmembrane #status predicted <TM6>  
 F:281-304/Domain: transmembrane #status predicted <TM7>

Query Match 36.7%; Score 723; DB 2; Length 355;  
 Best Local Similarity 43.5%; Pred. No. 1.5e-56;  
 Matches 131; Conservative 59; Mismatches 103; Indels 8; Gaps 3;

Qy 25 DWDYGAPOCKHDKVQTKQAGQLPLPLSIVFIFGVGNMLLVLLIJCNRKLKCLTDIYLNL 84  
 Db 18 DFMSGFCFESIVRAFGLPLPLSIVFIFGVGNMLLVLLIJCNRKLKCLTDIYLNL 84  
 Qy 85 AISDLFLPLTILPLWA-HSAANNEWFGNAMCKLKFGLTHIGHYFGGIFFLITIDRYLAIV 143  
 Db 78 AISDLFLPLSTLPFWVDYIMKGDWIFGNAMCKEVSGEYLGYSDFMEFTTLTLTIDRYLAIV 137  
 Qy 144 HAVFALKARTVFGVVTSVTPWLUVAYFAASVPGILIFTKQKEDSVYVGCPYFP 195  
 Db 138 HVVFALRARTVFGISSLITIWVLAALVSPICLVYEQSMETPYHTCRAILRKSLIRFL 197  
 Qy 200 NFHTIMRNLLGVLVPLIMIVCYSGILKTLRCNEKKHRARVVISITIMIVYFLFWTPY 259  
 Db 198 REFAQTMNLGVLVPLIMIVCYSGILKTLRCNEKKHRARVVISITIMIVYFLFWTPY 259  
 Qy 260 NIVILLNTQQEFFGLNSCESTSQLDQATOVTETLGTHCCINPITYAFVGKEKR 313  
 Db 257 YLAFAVSAFEVLYFTPSCLRSQQVDSLMIATELAYTHCCVNPVITYAFVGKEF 310  
 Qy 313 R 313  
 Db 308 K 308

**RESULT 12**  
 JC5067 G protein-coupled receptor CKR-L1 - human  
 N:Alternate names: chemokine receptor-like protein TER1; GPR CY6  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jul-2000  
 R:Zaballos, A.; Varon, R.; Gutierrez, J.; Lind, P.; Marquez, G.  
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996  
 A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes  
 A:Reference number: JC5067; MUID:97040707; PMID:8886020  
 A:Accession: JC5067  
 A:Molecule type: DNA  
 A:Residues: 1-355 <BOND>  
 A:Cross-references: EMBL:779782; NID:91668735; PID:CA02142.1; PID:91668736  
 R:Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.  
 Submitted to the EMBL Data Library, June 1996  
 A:Accession number: H01714  
 A:Status: translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA

Query Match 35.8%; Score 704.5; DB 2; Length 354;

|  |  |
|--|--|
| Best Local Similarity 47.6%; Pred. No. 6.6e-55; Matches 151; Conservative 43; Mismatches 112; Indels 11; Gaps 6; | Db 126 DRYLAIVLAAANSMMNRVYQHGVTLISGWAAAIIYVAAPQEMFTK-QKENE--CLGDPY 181       |
| QY 24 FDYDGA-PCHKEPDVKQIGAOLPPLYSLETFVGVMNLVVLILINGKKLKCLTDIYL 82  | QY 197 GWNFHFTMRN1----LGIVLPPLIMVICYSGILKTLRCRNEKKHRRAVRYIFTIMIVY 252        |
| Db 13 FEYDDSAEACYLGDIVAGTSLTISFYSIYVFTGLGVMLVYALTNSRSKSITDIYL 72   | Db 182 VLIQEIPWVIRNEINFGLFLPLMSYCVERIQTFLFSEKNHRRKA-KAIKLILLVVIE 240         |
| QY 83 NLAISDLFLITPLWAHSAAANEWVGAMCKLFGLTHIGYGGTFLFILLTIDRYLAI 142  | QY 253 FLFWTPNIVYLILNTFOEEFGLSNCESTSOLDQATQVTEFLGMHCCINPLIYAFVGEKF 312       |
| Db 73 NLAISDLFLITPLWAHSAAANEWVGAMCKLFGLTHIGYGGTFLFILLTIDRYLAI 132  | Db 241 FLFWTPNIVYLILNTFOEEFGLSNCESTSOLDQATQVTEFLGMHCCINPLIYAFVGEKF 300       |
| QY 143 VHAFVAKARTVTPEGVTSVITWLAVFASVPGPLIFTCKQEDSVYVCGPYFPRGWNNFH 202  | QY 313 RS-LFHIALGCRIPALQPKVCG 333  |
| Db 133 VLAANSMMNRVYQHGVTLISGWAAAIIYVAAPQEMFTK-RKDNE---CLGDPYDEVLQEIW 188   | Db 301 RRYLYHYGKCLAV-----LCG 317   |
| QY 203 TIMR----NILGLYPLIMVICYSGILKTLRCRNEKKHRRAVRYIFTIMIVYFLFWTP 258   | RESULT 15  |
| Db 189 PVLRNSEVNIGFLPVPLIMSFCYFRITVRLFLSCNKRNRA-RAIRLILVYVVFELFWTP 247   | JC5942   |
| QY 259 YNIVLILNTFOEFGLGSNCESTSOLDQATQVTEFLGMHCCINPLIYAFVGEKFERS-DEH 317  | C;Species: Homo sapiens (man)  |
| Db 248 YNIVLILNTFOEFGLGSNCESTSOLDQATQVTEFLGMHCCINPLIYAFVGEKFERS-DEH 307  | C;Accession: JG5942  |
| QY 318 IALGCRIPALQPKVCGG 334   | R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.    |
| Db 308 LYNKCLAVLCLGRPVHAG 324  | Biochem. Biophys. Res. Commun. 243, 264-268, 1998                            |
| JC404  | A;Title: Cloning and characterization of a novel human chemokine receptor.   |
| orphin G protein-coupled receptor - human  | A;Reference number: JG5942; MUID:98139902; PMID:9473515                      |
| N;Alternative names: V28 protein   | A;Accession: JC5942  |
| C;Species: Homo sapiens (man)  | A;Status: preliminary  |
| C;Accession: JG4304  | A;Molecule type: DNA   |
| R;Report: C.J.; Schweikart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.  | A;Residues: 1-344 <PAN>  |
| Gene 163, 295-299, 1995  | A;Cross-references: GB:U97123; NID:92897070; PIDN: AAC39595..1; PID:92897071 |
| A;Title: The orphan G-protein coupled receptor-encoding gene V28 is closely related to 9                         | C;Superfamily: vertebrate rhodopsin  |
| A;Reference number: JC4304; MUID:96011651; PMID:7590284  | Query Match Score 32.7%; Best Local Similarity 39.9%; Length 344;            |
| A;Accession: JC4304  | Matches 132; Conservative 58; Mismatches 120; Indels 21; Gaps 6;             |
| A;Molecule type: mRNA  | Query Match Score 32.7%; Best Local Similarity 39.9%; Pred. No. 1.4e-49;     |
| A;Residues: 1-355 <RGP>  | Matches 132; Conservative 58; Pred. No. 1.4e-49;                             |
| A;Cross-references: GB:U20350; PIDN:AAA91783..1; PID:96655801  | Db 23 DAEAQCDKYDAQASALQVLPSCASVFIGVLDLNLVLLVYKGUKRVENITYLNLAV 82             |
| A;Experimental source: peripheral blood mononuclear cell   | QY 27 DYGAPKHFVDVKQIGAQOLPPLPSLVIIFGFVGNMILVFLCNCKKLKCLTDIYLNLAV 86          |
| C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals                        | Db 87 SDDLFLLITPLWAHSAAANEWVGAMCKLFGLTHIGYGGTFLFILLTIDRYLAHV-A 145           |
| C;Genetics:  | Db 83 SNLCEFLLTPWHAHG-----GDPCKKLLIGLYFGLYSETFENCLLTWORYLVFLHKG 136          |
| A;Gene: v28  | QY 146 VFALKARTVIFGVTSVITWLAVFASVPGLILITKQKEDSVYVCGC---PYPPRG---W 198        |
| A;Map position: 3pter-p21  | Db 137 NFFSARRRVPDCGITSVLAINTVATLATLPEVYVYKQMEDQKYKCAFSRTFLPADETFW 196       |
| C;Superfamily: vertebrate rhodopsin  | QY 199 NNFHTIMRNTLGLVPLIMVICYSGILKTLRCRNEKKHRRAVRYIFTIMIVYFLFWTP 258         |
| C;Comments:  | Db 197 KHFLTKMNISVYLPFLFIFTFLFLVYOMRKTL--RFREQRYSFLKLVFAIMVFLMWAP 253        |
| F;66-88/Domain: transmembrane #status predicted <TM1>  | QY 259 YNIVLILNTFOEFGLGSNCESTSOLDQATQVTEFLGMHCCINPLIYAFVGEKFERS---- 314      |
| F;104-125/Domain: transmembrane #status predicted <TM2>  | Db 254 YNIAFFLSTFEHFSLSDCKSYNLDSVHTKLIATTHCCINPLIYAFLDTGFSKYLCR 313          |
| F;197-217/Domain: transmembrane #status predicted <TM4>  | QY 315 LFHIALGCRIPALQPKVCGGSGVRPGKNVKV 345                                   |
| F;230-254/Domain: transmembrane #status predicted <TM5>  | Db 314 CFHLRSNTPLQPRGOSAQGTSREEPDHSTEV 344                                   |
| F;275-296/Domain: transmembrane #status predicted <TM6>  | Search completed: May 19, 2003, 16:49:15<br>Job time : 30.0436 secs          |
| Query Match Score 35.4%; Best Local Similarity 4.53%; Length 355;  |  |
| Matches 146; Conservative 49; Mismatches 111; Indels 16; Gaps 7;   |  |
| QY 18 EEVTFDFDY-DYGCHKFVDVKQIGAQOLPPLPSLVIIFGFVGNMILVFLCNCKKLKCL 76  |  |
| Db 6 ESVTFENFYDDLAECYIGDIVVFTGLTVLFLSIFYSVIAIGLVNLVVFALTNSKKPKSV 65  |  |
| QY 77 TDIVLNLALSDLFLITPLWAHSAAANEWVGAMCKLFGLTHIGYGGTFLFILLTIDRYLTI 136   |  |
| Db 66 TDIVLNLALSDLFLITPLWAHSAAANEWVGAMCKLFGLTHIGYGGTFLFILLTIDRYLTI 125   |  |
| Qy 137 DRYLAIVLAAANSMMNRVYQHGVTLISGWAAAIIYVAAPQEMFTK-QKENE--CLGDPY 196   |  |

